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Astraeus ryoocheoninii sp. nov. from Korea and Japan and phylogenetic relationships within *Astraeus*

Rhim Ryoo[1*], Hong-duck Sou[2], Hyun Park[3] & Kang-Hyeon Ka[1]

[1] *Division of Wood Chemistry and Microbiology, National Institute of Forest Science, Seoul 02455, Republic of Korea*

[2] *Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo 1138657, Japan*

[3] *Division of Global Forestry, National Institute of Forest Science, Seoul 02455, Republic of Korea*

[*] Correspondence to: *rryoo@korea.kr*

Abstract—The morphological characteristics of a collection by C.I. Ryoo and K.-H. Ka from the demilitarized zone (DMZ) of Korea, invalidly published as "*Astraeus koreana*", are re-evaluated, described, and illustrated. Phylogenetic analysis using nrITS sequence data indicate that "*Astraeus koreana*", an unnamed "Japanese *Astraeus* group 2", and a Japanese specimen E0059827 all differ from *A. hygrometricus* var. *koreanus* and represent a new species, proposed here as *Astraeus ryoocheoninii*.

Key words—basidiospore, ornamentations, peridium, ectomycorrhiza

Introduction

Species of *Astraeus* are ectomycorrhizal and form symbiotic associations with various tree species in the genera *Alnus*, *Castanea*, *Eucalyptus*, *Pinus*, and *Pseudotsuga* (Malajczuk et al. 1982, Molina 1979, Nouhra & Domínguez 1998, Trappe 1967). Mycorrhizal synthesis studies have been conducted to confirm their host specificity in the field (Danielson 1984; Petcharat 2005; Molina 1979, 1981; Molina & Trappe 1982). Mycorrhizae carry out the efficient recycling of nutrients between roots of host plant and fungi in soil (Malajczuk et al. 1982). *Astraeus* species are also economically important as they are collected for sale in commercial markets as edible mushrooms (Maiti et al. 2008).

Astraeus (*Sclerodermatineae, Boletales*, *Agaricomycetes*) was originally described by Morgan (1889). The genus contains seven widely distributed species (http://www.mycobank.org) and has been recorded from Australasia, Africa, Asia, Europe, and North and South America (Coker & Couch 1928, Cunningham 1944, Dring 1964, Imazeki & Hongo 1989, Liu 1984, Nouhra & Domínguez 1998, Wilson et al. 2012). The type species, *A. hygrometricus* (Pers.) Morgan, was originally described in *Geastrum*; a Korean variety has been described as *A. hygrometricus* var. *koreanus* V.J. Staněk [≡ *A. koreanus* (V.J. Staněk) Kreisel] (Staněk 1958, Kreisel 1976). Several new *Astraeus* species have been described recently from Asia: *A. asiaticus* Phosri et al., *A. odoratus* Phosri et al. [= *A. thailandicus* Petcharat], and *A. sirindhorniae* Watling et al. (Petcharat 2005; Phosri et al. 2004, 2007, 2014). Recently *Astraeus hygrometricus* var. *koreanus* and an unnamed *Astraeus* taxon from Japan ("Clade VII, Japanese *Astraeus* group 2" of Fangfuk et al. 2010) were morphologically and molecularly re-evaluated (Fangfuk et al. 2010). However, their relationship was left unresolved, and Fangfuk et al. (2010) concluded that further studies were necessary to determine the phylogenetic position of var. *koreanus* and the identification of "Japanese *Astraeus* group 2."

Until 2001, *Astraeus* was largely defined by two species, *A. hygrometricus* and *A. pteridis* (Kirk et al. 2001, Zeller 1948). Since then several new species have been described using morphological characteristics and molecular methods (Phosri et al. 2004, 2007; Fangfuk et al. 2010). *Astraeus asiaticus* and *A. odoratus* were described as phylogenetically distinct from *A. pteridis*. SEM was used to characterize basidiospore ornamentation as a character in a taxonomic key of the genus. Phosri et al. (2007) suggested that the *A. hygrometricus* complex forms a polyphyletic group in ITS rDNA sequence analyses. These studies showed that in *Astraeus* phylogenetic clades largely correlate with geographical areas. Fangfuk et al. (2010) also confirmed polyphyletic relationships within *Astraeus*.

From 1995 to 2000, researchers from NIFoS (National Institute of Forest Science) conducted an ecological investigation in the Korean demilitarized zone (DMZ) including the civilian control zone (CCZ). In 1998, an undetermined *Astraeus* species was collected from the DMZ, described, and photographed by C.I. Ryoo and K.-H. Ka. This collection was named "*A. koreana*" by Ryoo et al. (1999), but the name was invalid because no Latin description was included and no type specimen was designated. "*Astraeus koreana*" is macro-morphologically similar to *A. hygrometricus* var. *koreanus* (Staněk 1958) and shares micro-morphological characteristics with "Japanese *Astraeus* group 2" (Fangfuk et al. 2010).

Our study taxonomically re-evaluated *A. hygrometricus* var. *koreanus*, "*A. koreana*", and "Japanese *Astraeus* group 2" by using phylogenetic analysis to

identify which morphological characteristics are important for distinguishing taxonomic boundaries. *Astraeus ryoocheoninii* is proposed as a new species incorporating "*Astraeus koreana*" and "Japanese *Astraeus* group 2".

Materials & methods

Morphological characteristics

We studied the macro-morphological characteristics of fresh material as recorded and photographed in 1998 by C.I. Ryoo & K.-H. Ka and their dried material conserved in the herbarium of National Institute of Forest Science, Hongnung Arboretum, Seoul, the Republic of Korea (KFI). Micro-morphological features were described from dried materials mounted in 3% KOH, Melzer's reagent, and cotton blue reagent under a Leica DM 2500 microscope using DIC optics. Basidiospore ornamentation was examined under a Hitachi S-3500N electron microscope using samples coated in platinum palladium at 10 kV.

Molecular analysis

DNA was extracted from dried material using the CTAB (cetyltrimethyl ammonium bromide) buffer method of Rogers & Bendich (1994). The rDNA ITS region was amplified by PCR using primers ITS1 and ITS4 (White et al. 1990). A 50 µl total volume per PCR reaction contained template DNA (1.2 µl), 10× buffer, 0.5 M KCl, 0.1 M Tris-HCl, 0.1 % Triton X-100, and 15 mM $MgCl_2$, 2.5 mM dNTP, 100 pM of each primer, and Taq polymerase (5 unit/µl). PCR thermal cycler protocols comprised 35 cycles of 30 sec at 94 °C, 30 sec at 56 °C, and 1 min at 72 °C with the first denaturation and last extension times extended to 5 min at 72 °C (Gardes & Bruns 1993). Cycle sequencing was performed using the primers ITS1 and ITS4 using BigDye™ cycle sequencing kit, version 3.1 (Applied Biosystems). Purified DNAs were directly sequenced on an ABI Prism TM 377 DNA automatic DNA Sequencer (Applied Biosystems).

Phylogenetic analysis

A total of 28 sequences, one newly extracted in this study and 27 retrieved from GenBank, were aligned using Clustal X (Thompson et al. 1997) implemented in the program MEGA v 5.05 (Tamura et al. 2011). Parsimony analyses were performed in PAUP* v 4.0b10 (Swofford 2002) with bootstrap statistics generated using a heuristic search with 1000 replicates, each with 10 random sequence additions, and TBR branch swapping. Bayesian analyses were performed in MrBayes v 3.1 (Ronquist & Huelsenbeck 2003) using 2,000,000 generations and 4 chains under the general time reversible (GTR) model with gamma-distributed substitution rates. Trees were saved every 100th generation, and the first 1000 of 2001 trees were discarded as the burn-in. A 50% majority rule consensus tree on treefiles from Bayesian and parsimony bootstrap analyses was used to compute posterior probabilities (PPs) and bootstrapping (BS) values respectively. The outgroup of *Scleroderma verrucosum* (Genbank AJ629886) and *Pisolithus* sp. (AJ629887) was used in the systematic dataset following the methods by Phosri et al. (2007). Sequences used in this study are listed in Table 1.

Table 1. List of *Astraeus*, *Pisolithus*, and *Scleroderma* sequences used in the phylogenetic analysis

Taxon	Country	Host plant	GenBank no.
A. asiaticus	Thailand	—	AJ629381
	Thailand	—	AJ629382
	Thailand	—	AJ629386
A. hygrometricus	USA	—	AJ629398
	USA	—	AJ629399
	USA	—	AJ629402
	USA	—	AJ629403
	Greece	—	AJ629404
	Spain	—	AJ629408
A. hygrometricus var. *koreanus*	Japan	*Pinus thunbergii*	AB535105
	Japan	*Pinus thunbergii*	AB535106
	Japan	*Pinus thunbergii*	AB535107
A. odoratus	Thailand	*Dipterocarpaceae*	AB507406
	Thailand	—	AB535108
	Thailand	*Dipterocarpaceae*	AB535113
	Thailand	*Dipterocarpaceae*	AJ629875
	Thailand	—	AJ629880
A. pteridis	USA	—	AJ629409
	USA	—	AJ629410
A. ryoocheoninii	**Korea**	***Pinus densiflora***	**KC985146**
	Japan	—	AB507397
	Japan	—	AB535109
	Japan	*Pinus densiflora*	AB535110
	Japan	*Quercus serrata*	AB535111
	Japan	*Quercus* sp.	AB535112
	Japan	*Carpinus laxiflora*	AJ629405
Pisolithus sp.	Thailand	—	AJ629887
S. verrucosum	Spain	—	AJ629886

Results

Phylogenetic analysis

Based on nrITS sequence data obtained in this study and from GenBank, phylogenetic placement and relationships of *Astraeus* taxa were inferred from the Bayesian and MP analyses. No difference was found between the topologies using different methodologies so only the results from the Bayesian analysis is shown (Fig. 1). The aligned dataset included 595 total characters, with 393 constant, 85 variable, and 117 parsimony informative in MP analysis. This dataset produced 1,000 trees with 315 steps of tree length, a consistency

index (CI) of 0.8349, a homoplasy index (HI) of 0.1651, and a retention index (RI) of 0.9091.

Five *Astraeus* clades are recognized in Bayesian and parsimony analyses (Fig. 1). Clade A, representing *A. hygrometricus*, is subdivided into three geographical subclades: North American (0.81 PP, 0.76% BS); South European (0.92 PP, 91% BS); and Japanese (0.80 PP, 83% BS); the Japanese subclade represents *A. hygrometricus* var. *koreana*, which is confirmed as a variety rather than a species as suggested by Kreisel (1976). Clade B, here named *A. ryoocheoninii*, includes "*A. koreana*", "Japanese *Astraeus* group 2",

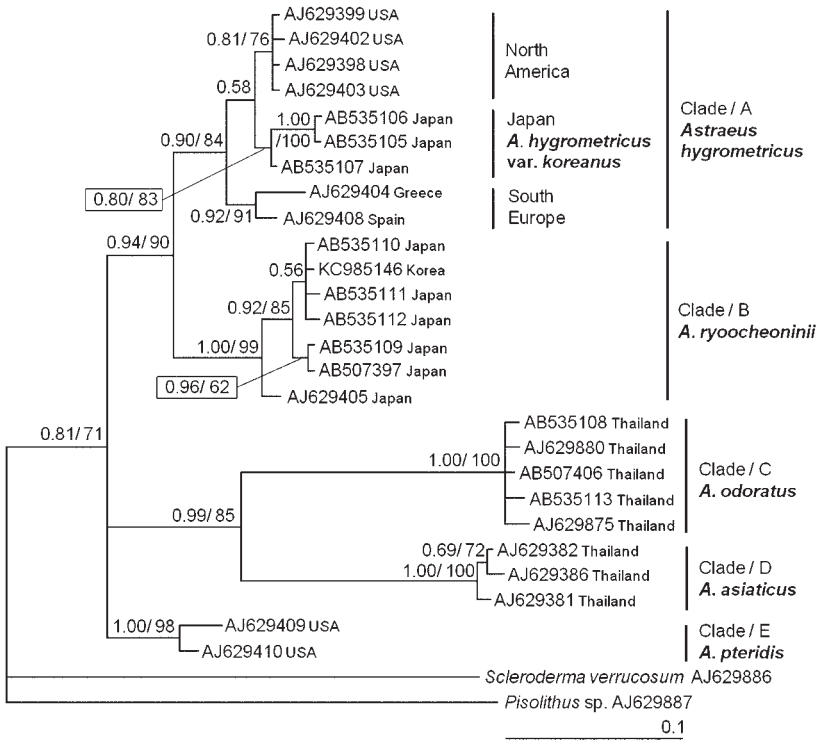

Fig. 1. Phylogenetic analysis for the genus *Astraeus* based on (ITS1+5.8S+ITS2) rDNA region. Bayesian consensus tree used to a 50% majority-rule carried out two million generations and four chains. Maximum parsimony analysis generated from 1000 replicates with 10 random addition sequences. Because no differences were found between the tree topologies from the two analyses, only the MCMC tree is shown. Numbers at each branch indicate posterior probability (left) and bootstrap support (right).

and Japanese specimen E00159827 (GenBank AJ629405) in a monophyletic clade (1.00 PP, 99% BS). The other three monophyletic clades represent: clade C—*A. odoratus* (1.00 PP, 100% BS); clade D—*A. asiaticus* (1.00 PP, 100% BS); and clade E—*A. pteridis* (1.00 PP, 98% BS).

Taxonomy

Astraeus ryoocheoninii Ryoo **sp. nov.** Fig. 2

MycoBank MB 804156

"*Astraeus koreana*" C.I. Ryoo, KMS Newsletter 11(2): 20, 1999, nom. inval.

"Japanese *Astraeus* group 2" Fangfuk et al., Mycoscience 51: 291–299, 2010.

Differs from *Astraeus hygrometricus* var. *koreanus* by its larger basidiomes and smaller basidiospores.

Type—The Republic of Korea, Central and Eastern mountainous region near the DMZ of Korea, Kosung, Mt. Hangrohbong, alt. ± 850 m, on sandy soil associated with *Pinus densiflora*, 20 July 1998, C.I. Ryoo & K.-H. Ka (**Holotype**, KFI-DMZ002 ; GenBank KC985146).

Etymology—Named in honour of mycologist, Dr. Cheon-In Ryoo.

Basidiome globose, rough, with an ostiole encircled by a cracked peridium 60–100 mm wide when mature; the exoperidium splitting longitudinally and re-curving into star-like rays, expanding when exposed to moisture and re-coiling towards gleba upon desiccation. Exoperidium slightly viscous, smooth, grayish brown, covering endoperidium, splitting into 15–19(–21) little, star-like rays that open when hydrated, upright at first, curving back, inner surface becoming distinctly cracked with irregular trapezoid and rhomboid patterns, closing in dry weather. Endoperidium a thin membranous layer of tissue, enclosing the spore mass in a 20–40 mm diameter sac, nearly round, with an irregularly shaped ostiole at top, surface felty rough, whitish, becoming gray to brown. Basidiospore mass whitish when young, brownish and powdery at maturity. Basidiospores globose, (5.3–)7.0–9.1(–9.5) µm in diameter (n = 48), (4.8–)5.0–9.0 µm in diameter without the ornamentation, chocolate dark brown, cell wall thickened, with spiny, moderately dense ornamentation with rounded (sometime spiked) top, (0.5–)0.6–1.3(–1.5) µm long, dark brown, negative reaction from 3% KOH, Melzer's reagent (inamyloid) and cotton blue reagent. Paracapillitium hyphae (4.0–)5.0–6.0(–6.5) µm in diameter, septate, with clamp-connection-like structures present on some septa.

Original description of "*Astraeus koreana*" (Ryoo et al. 1999): "These specimens were characterized by having the inner surface of the exoperidium distinctly cracked in irregular patterns, numerous, 15–19(–21) rays and 5.7–9.3 µm average size of basidiospores with short, moderately dense ornamentation, growing symbiotic in association with *Pinus densiflora*. Korean common name of these taxa were called as Seonbi-meonji-beoseos."

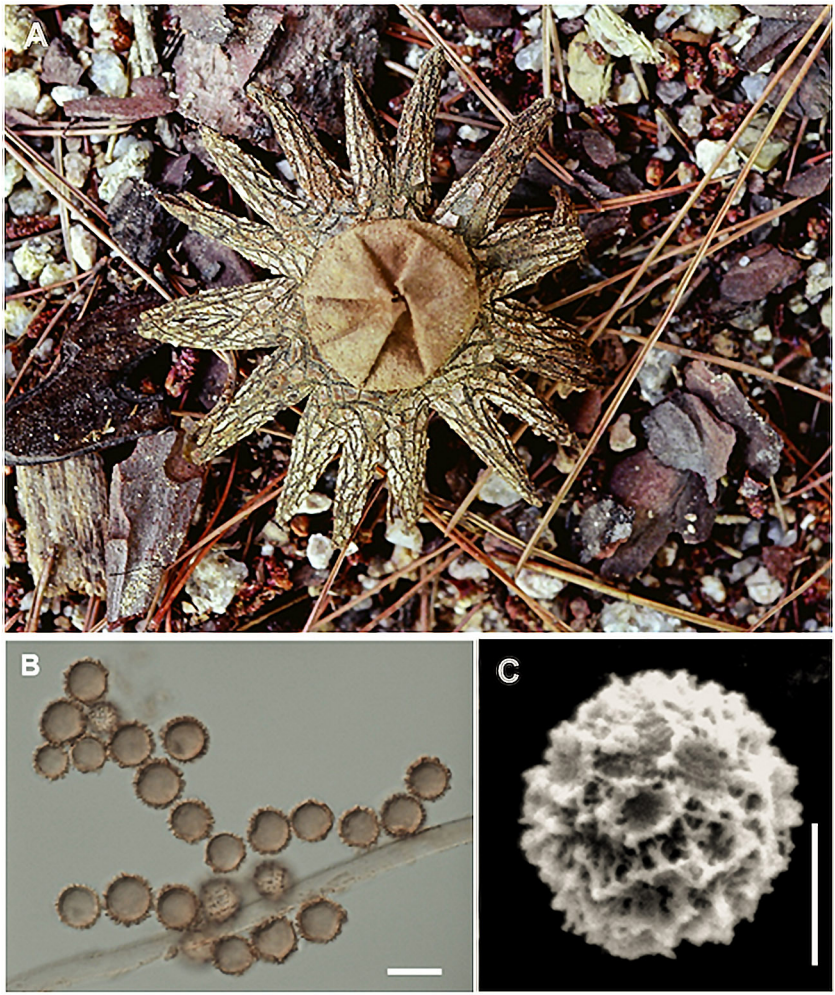

Fig. 2. *Astraeus ryoocheoninii* (KFI-DMZ002, holotype). A. basidiomata; B. basidiospores under DIC microscope; C. basidiospores under SEM. Scale bars: B = 10 µm; C = 5 µm

Additional specimens—Japanese specimens now included in *A. ryoocheoninii* were listed and described in Phosri et al. (2007, as ASTRAE_94 = E00159827, GenBank AJ629405), and in Fangfuk et al. (2010, as "Japanese *Astraeus* group 2").

Comments — The Japanese specimens of *Astraeus ryoocheoninii* agree with the Korean holotype description in basidiospore size and dense ornamentation with short spines (Table 2).

Table 2. Comparison of taxonomic characteristics of *Astraeus hygrometricus* and Asian *Astraeus* species

Taxon	Acute rays	Spore size (µm)	Spore ornamentation	Clade
A. hygrometricus	6–15[a]	5.2–13.9[a]	Dense, narrow, 0.7–1.3 µm[b]	A
A. hygrometricus var. *koreanus*	15–22[a]	7.6–12.9[a]	Tightly dense, narrow, 0.8–1.6 µm[a]	A
A. ryoocheoninii – "*A. koreana*"	15–21	5.3–9.5	Slightly dense, 0.6–1.3 µm	B
A. ryoocheoninii – "*Astraeus* group 2"	5–13[a]	5.2–9.6[a]	Moderately dense, 0.6–1.7 µm[a]	B
A. ryoocheoninii – AJ629405	—	6.8–9.0[a]	Dense, 0.8–1.6 µm[b]	B
A. odoratus	3–9[c]	7.5–15.2[c]	Moderately dense, narrow, 1.0–1.7 µm[c]	C
A. asiaticus	5–12[b]	8.8–15.2[b]	Very dense, 0.9–1.45 µm[b]	D

[a] Fangfuk et al. (2010); [b] Phosri et al. (2007); [c] Phosri et al. (2004).

The *A. ryoocheoninii* holotype is similar to *A. hygrometricus* var. *koreanus* in the high number of split acute rays, but *A. hygrometricus* var. *koreanus* differs by its larger basidiospores with longer, denser ornamentation (Table 2), much smaller basidiocarps (15–20 mm), and much thinner endoperidium (10–15 mm; Staněk 1958; Imazeki & Hongo 1989; Fangfuk et al. 2010). The type locality of *A. ryoocheoninii* was a warm, dry locality associated with stands of Korean red pine (*Pinus densiflora*) on sandy soil, whereas the type locality of *A. hygrometricus* var. *koreanus* was a stony plateau with an eastern orientation among dwarf-oaks and scattered pines in the mountains of North Korea (Staněk 1958: 632, 819).

The two Thai species, *A. odoratus* and *A. asiaticus*, have larger basidiospores and fewer cracked rays than *A. ryoocheoninii* (Table 2). The basidiospore spines of *A. odoratus* are narrower, more coalescent, and less densely arranged than those of *A. ryoocheoninii* (Phosri et al. 2004, 2007; Table 2).

Discussion

The studies of Phosri et al. (2007) and Fangfuk et al. (2010) resolved several questions concerning the phylogenetic relationships of the *Astraeus* species. The present study uses ITS rDNA variation to establish the systematic relationship among *A. hygrometricus* var. *koreanus*, "*A. koreana*", and "Japanese *Astraeus* group 2", and to identify morphological characteristics

that can be used to identify these species. This study suggests that *Astraeus hygrometricus* var. *koreanus* should be recognized at the rank of variety within the *A. hygrometricus* complex, rather than at specific rank as proposed by Kreisel (1976). The new species *Astraeus ryoocheoninii* is described for the well-supported clade that includes the sequences of "*A. koreana*", "Japanese *Astraeus* group 2", and Japanese specimen E00159827 (GenBank AJ629405), previously loosely associated with *A. hygrometricus* by Phosri et al. 2007 and with "Japanese *Astraeus* group 1" by Fangfuk et al. 2010).

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